Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-11 (cancelled)

12. (Currently amended) A method for generating a secondary library of secondary protein variants of a target protein comprising:

a) inputting the three dimensional coordinates of said target protein into a computer;

b) determining a criteria for including favorably ranked primary variant proteins for a primary library;

~~b~~c) utilizing a force field calculation to generate ~~a~~ said primary library comprising a plurality of favorably ranked primary variant proteins comprising ~~primary~~ variant amino acid residues at ~~primary~~ variant positions;

d) determining a criteria for selecting amino acid residues from each of said variant positions from said favorably ranked primary variant proteins

e) selecting amino acid residues from a plurality of said variant positions from said favorably ranked primary variant proteins; and

~~c~~f) combining a plurality of said ~~primary variant~~ selected amino acid residues ~~from step~~ b) to generate a said secondary library of said secondary variant proteins, wherein at least one of said secondary variant proteins is different from ~~the~~ said primary variant proteins.

13. (Previously presented) A method according to claim 12, wherein said force field calculation is a Self-Consistent Mean Field (SCMF) calculation.

Claims 14-20 (Cancelled)

21. (Currently amended) A method according to claim 12, further comprising synthesizing a plurality of said secondary variant proteins, wherein said combining comprises:

eg) generating a set of oligonucleotide probes each encoding at least one of said ~~primary variant~~ amino acid residues at said variant positions;

fh) using said probes in a polymerase chain reaction (PCR) to generate a plurality of oligonucleotide sequences, each encoding said secondary variant sequences; and

~~g~~i) producing said secondary variant sequences in host cells transformed with said oligonucleotide sequences.

22. (Previously presented) A method according to claim 21 wherein said PCR is multiple PCR wherein said probes are pooled.

23. (Previously presented) A method according to 22 wherein said probes are added in equimolar amounts.

24. (Currently amended) A method according to claim 22 wherein said probes are combined in amounts that correspond to the frequency of the said ~~variant~~ amino acid residues at said variant positions in said secondary library.

Claims 25-32 (cancelled)

33. (Currently amended) A method for generating a secondary library of secondary protein variants of a target protein comprising:
a) inputting the three dimensional coordinates of said target protein into a computer;
b) determining a criteria for including favorably ranked primary variant proteins for a primary library;
bc) utilizing a force field calculation to generate a primary library of favorably ranked primary variant proteins comprising a plurality of ~~primary~~ variant amino acid residues at ~~primary~~ variant positions;
d) determining a criteria for selecting amino acid residues from each of said variant positions from said favorably ranked primary variant proteins
e) selecting amino acid residues from a plurality of said variant positions from said favorably ranked primary variant proteins; and
ef) combining a plurality of said ~~primary variant~~ selected amino acid residues from a plurality of said variant positions from said favorably ranked primary variant proteins ~~step b)~~ to generate a secondary library of secondary variant proteins.

34. (Currently amended) A method for generating a secondary library of secondary protein variants of a target protein comprising:
a) inputting the three dimensional coordinates of said target protein into a computer;
b) determining a criteria for including favorably ranked primary variant proteins for a primary library;